Access DB# _____ /

SEARCH REQUEST FORM
Scientific and Technical Information Center

(Mailbox 12E12)

Requester's Full Name: _Anne-Marie Baker_   Examiner # : _74977_ Date: _4/18/01_
Art Unit: _1632_   Phone Number 30_6-9155_   Serial Number: _08/963,288_
Mail Box and Bldg/Room Location: _12D07_   Results Format Preferred (circle): (PAPER) DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _Expression Vector_

Inventors (please provide full names): _Norstedt et al_

Earliest Priority Filing Date: _10/19/95_

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- Please perform an ~~oligo~~ search for
  TTCTGAGAA .
  Limit to 12 nur or smaller.

POINT OF CONTACT:
BARB O'BRYEN
TECH. INFORMATION SPECIALIST
STIC   CM1 12C14   308-4291

- Claim is directed to an enhancer element consisting essentially of the nucleotide sequence.

- There is no CRF for this and thus no SEQ ID No. $ for this 9-nucleotide sequence because the sequence rules apply to sequences 10-nucleotides or longer. Thus, this case is not required to comply with the sequence rules. Or, looked at another way, the case is in compliance because no CRF is required.

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _BSB_	NA Sequence (#) _1_	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _4-18-01_	Bibliographic _____	Dr.Link _____
Date Completed: _4-23-01_	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _20_	Fulltext _____	Sequence Systems _IG, GA abss03_
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _15_	Other _____	Other (specify) _____

PTO-1590 (1-2000)

BAK

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Amz

Qy   1 ttctgagaa 9
        |||||||||
Db   9 TTCTGAGAA 1

RESULT 2
US-08-369-796-34/c
Sequence 34, Application US/0836979G
Patent No. 5716622
GENERAL INFORMATION:
;   APPLICANT: James E. Darnell, Jr.
;   APPLICANT: Zilong Wen
;   APPLICANT: Curt M. Horvath
;   APPLICANT: Zhong Zhong
;   TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;   TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Klauber & Jackson
;   STREET: 411 Hackensack Avenue
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/369,796
;   FILING DATE: 06-JAN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 600-1-116
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201 487-5800
;   TELEFAX: 201 343-1684
;   TELEX: 13521
INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear

US-08-369-796-34

Query Match   100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+07;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ttctgagaa 9
        |||||||||
Db   9 TTCTGAGAA 1

RESULT 3
US-08-410-779B-35/c
Sequence 35, Application US/08410779B
Patent No. 5814517
GENERAL INFORMATION:
;   APPLICANT: SEIDEL, H. MARTI
;   APPLICANT: LAMB, I. PETER
;   TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
;   TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
;   NUMBER OF SEQUENCES: 166
;   CORRESPONDENCE ADDRESS:

;   ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
;   STREET: 9393 TOWNE CENTRE DRIVE
;   CITY: SAN DIEGO
;   STATE: CALIFORNIA
;   ZIP: 92121
;   COUNTRY: US
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/410,779B
;   FILING DATE: 27-MAR-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/228,935
;   FILING DATE: 14-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: JURGENSEN, THOMAS E
;   REGISTRATION NUMBER: 34,195
;   REFERENCE/DOCKET NUMBER: 016-0013A.US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 550-7675
;   TELEFAX: (619) 535-3906
INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
;   DESCRIPTION: SYNTHETIC DNA"
US-08-410-779B-35

Query Match   100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+07;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ttctgagaa 9
        |||||||||
Db   9 TTCTGAGAA 1

RESULT 4
US-08-852-091-34/c
Sequence 34, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
;   APPLICANT: James E. Darnell, Jr.
;   APPLICANT: Zilong Wen
;   APPLICANT: Curt M. Horvath
;   APPLICANT: Zhong Zhong
;   TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;   TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Klauber & Jackson
;   STREET: 411 Hackensack Avenue
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/852,091
;   FILING DATE: 06-MAY-1997

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OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: April 21, 2001, 12:13:27 ; Search time 80.36 Seconds
                 (without alignments)
                 19.555 Million cell updates/sec

Title: SHORT
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 23618

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	9	100.0	9	1	US-08-411-020-13	Sequence 13, Appl
c 2	9	100.0	9	1	US-08-369-796-34	Sequence 34, Appl
c 3	9	100.0	9	1	US-08-411-779B-35	Sequence 35, Appl
c 4	9	100.0	9	1	US-08-852-091-34	Sequence 34, Appl
c 5	9	100.0	9	5	PCT-US95-04477-35	Sequence 35, Appl
c 6	9	100.0	9	5	PCT-US95-17025-34	Sequence 34, Appl
c 7	8	88.9	10	1	US-08-440-787A-85	Sequence 85, Appl
c 8	8	88.9	10	1	US-08-440-787A-86	Sequence 86, Appl
c 9	8	88.9	10	1	US-08-268-799-3	Sequence 3, Appl
c 10	7.4	82.2	9	1	US-08-411-020-12	Sequence 12, Appl
c 11	7.4	82.2	9	1	US-08-411-020-13	Sequence 13, Appl
c 12	7.4	82.2	9	1	US-08-369-796-34	Sequence 34, Appl
c 13	7.4	82.2	9	1	US-08-369-796-31	Sequence 31, Appl
c 14	7.4	82.2	9	1	US-08-369-796-36	Sequence 36, Appl
c 15	7.4	82.2	9	1	US-08-369-796-35	Sequence 35, Appl
c 16	7.4	82.2	9	1	US-08-410-779B-35	Sequence 35, Appl
c 17	7.4	82.2	9	1	US-08-410-779B-31	Sequence 31, Appl
c 18	7.4	82.2	9	1	US-08-410-779B-51	Sequence 51, Appl
c 19	7.4	82.2	9	1	US-08-410-779B-35	Sequence 35, Appl
c 20	7.4	82.2	9	1	US-08-852-091-31	Sequence 31, Appl
c 21	7.4	82.2	9	1	US-08-852-091-31	Sequence 31, Appl
c 22	7.4	82.2	9	1	US-08-852-091-34	Sequence 34, Appl
c 23	7.4	82.2	9	1	US-08-852-091-36	Sequence 36, Appl
c 24	7.4	82.2	9	1	US-08-852-091-38	Sequence 38, Appl
c 25	7.4	82.2	9	2	US-08-873-709-6	Sequence 6, Appl
c 26	7.4	82.2	9	5	PCT-US95-04477-31	Sequence 31, Appl
c 27	7.4	82.2	9	5	PCT-US95-04477-35	Sequence 35, Appl
c 28	7.4	82.2	9	5	PCT-US95-04477-51	Sequence 51, Appl
c 29	7.4	82.2	9	5	PCT-US95-04477-51	Sequence 51, Appl
c 30	7.4	82.2	9	5	PCT-US95-17025-31	Sequence 31, Appl
c 31	7.4	82.2	9	5	PCT-US95-17025-34	Sequence 34, Appl
c 32	7.4	82.2	9	5	PCT-US95-17025-36	Sequence 36, Appl
c 33	7.4	82.2	9	5	PCT-US95-17025-38	Sequence 38, Appl
c 34	7.4	82.2	10	1	US-08-410-779B-53	Sequence 53, Appl
c 35	7.4	82.2	10	1	US-08-410-779B-53	Sequence 53, Appl
c 36	7.4	82.2	10	5	PCT-US95-04477-53	Sequence 53, Appl
c 37	7.8	77.8	11	1	US-08-394-191-9	Sequence 9, Appl
c 38	7.8	77.8	11	1	US-08-458-364-9	Sequence 9, Appl
c 39	7.8	77.8	11	1	US-09-177-431-17	Sequence 17, Appl
c 40	7.8	77.8	11	3	US-08-525-506-8	Sequence 8, Appl
c 41	7.8	77.8	11	5	US-08-859-954-516	Sequence 516, App
c 42	7.8	77.8	8	3	US-09-085-028-8	Sequence 8, Appli
c 43	7.8	77.8	8	4	US-08-222-177A-410	Sequence 410, App
c 44	7	77.8	10	1	US-08-222-177A-410	Sequence 410, App
c 45	7	77.8	11	2	US-08-232-016-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-411-020-13/c
; Sequence 13, Application US/08411020
; Patent No. 5712094
; GENERAL INFORMATION:
;   APPLICANT: SEIDEL, H. MARTI
;   APPLICANT: LAMB, I. PETER
;   APPLICANT: CHAN, SHIN-SHAY TIAN
;   TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
;   TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ligand Pharmaceuticals Incorporated
;   STREET: 9393 Towne Centre Drive
;   CITY: San Diego
;   STATE: California
;   COUNTRY: US
;   ZIP: 92121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/411,020
;   FILING DATE: 27-MAR-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jurgensen, Thomas E.
;   REGISTRATION NUMBER: 34,195
;   REFERENCE/DOCKET NUMBER: 016-0030.US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 550-7675
;   TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
;   DESCRIPTION: SYNTHETIC DNA"
US-08-411-020-13

  Query Match   100.0%; Score 9; DB 1; Length 9;
  Best Local Similarity   100.0%; Pred. No. 1.9e+07;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ttctgagaa 9
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Db   9 TTCTGAGAA 1

RESULT 2
US-08-369-796-34/c
Sequence 34, Application US/08369796
Patent No. 5716622
GENERAL INFORMATION:
    APPLICANT: James E. Darnell, Jr.
    APPLICANT: Zilong Wen
    APPLICANT: Curt M. Horvath
    APPLICANT: Zhong Zhong
    TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
    NUMBER OF SEQUENCES: 39
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Klauber & Jackson
        STREET: 411 Hackensack Avenue
        CITY: Hackensack
        STATE: New Jersey
        COUNTRY: USA
        ZIP: 07601
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/369,796
        FILING DATE: 06-JAN-1995
        CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
        NAME: Jackson Esq., David A.
        REGISTRATION NUMBER: 26,742
        REFERENCE/DOCKET NUMBER: 600-1-116
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 201 487-5800
        TELEFAX: 201 343-1684
        TELEX: 133521
    INFORMATION FOR SEQ ID NO: 34:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 9 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: double
            TOPOLOGY: linear
        MOLECULE TYPE: DNA synthetic probe
        ANTI-SENSE: NO
US-08-369-796-34

Qy   1 ttctgagaa 9
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Db   9 TTCTGAGAA 1

Query Match   100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+07;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-410-779B-35/c
Sequence 35, Application US/08410779B
Patent No. 5814517
GENERAL INFORMATION:
    APPLICANT: LAMB, I. PETER
    APPLICANT: SEIDEL, H. MARTI
    TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
    TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
    NUMBER OF SEQUENCES: 166
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
        STREET: 9393 TOWNE CENTRE DRIVE
        CITY: SAN DIEGO
        STATE: CALIFORNIA
        COUNTRY: US
        ZIP: 92121
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/410,779B
        FILING DATE: 27-MAR-1995
        CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/228,935
        FILING DATE: 14-APR-1994
    ATTORNEY/AGENT INFORMATION:
        NAME: JURGENSEN, THOMAS E
        REGISTRATION NUMBER: 34,195
        REFERENCE/DOCKET NUMBER: 016-0013A.US
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (619) 550-7675
        TELEFAX: (619) 535-3906
    INFORMATION FOR SEQ ID NO: 35:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 9 base pairs
            TYPE: nucleic acid
            STRANDEDNESS: single
            TOPOLOGY: linear
        MOLECULE TYPE: other nucleic acid
            DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
            DESCRIPTION: SYNTHETIC DNA"
US-08-410-779B-35

Qy   1 ttctgagaa 9
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Db   9 TTCTGAGAA 1

Query Match   100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+07;
Matches   9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-08-852-091-34/c
Sequence 34, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
    APPLICANT: James E. Darnell, Jr.
    APPLICANT: Zilong Wen
    APPLICANT: Curt M. Horvath
    APPLICANT: Zhong Zhong
    TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
    NUMBER OF SEQUENCES: 39
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Klauber & Jackson
        STREET: 411 Hackensack Avenue
        CITY: Hackensack
        STATE: New Jersey
        COUNTRY: USA
        ZIP: 07601
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/852,091
        FILING DATE: 06-MAY-1997

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;         CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 08/369,796
;         FILING DATE: 06-JAN-1995
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Jackson Esq., David A.
;         REGISTRATION NUMBER: 26,742
;         REFERENCE/DOCKET NUMBER: 600-1-116
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 201 487-5800
;         TELEFAX: 201 343-1684
;         TELEX: 133521
;   INFORMATION FOR SEQ ID NO: 34:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 9 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: double
;         TOPOLOGY: linear
;       MOLECULE TYPE: DNA synthetic probe
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
  US-08-852-091-34

Qy        Query Match    100.0%; Score 9; DB 2; Length 9;
Db        Best Local Similarity 100.0%; Pred. No. 1.9e+07;
          Matches  9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy  1 ttctgagaa 9
       |||||||||
Db  9 TTCTGAGAA 1


RESULT 5
PCT-US95-04477-35/c
Sequence 35, Application PC/US9504477
;   GENERAL INFORMATION:
;       APPLICANT:
;       TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
;       TITLE OF INVENTION: CYTOKINES AND METHODS FOR THEIR USE
;       NUMBER OF SEQUENCES: 165
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: PCT/US95/04477
;         FILING DATE:
;         CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/228,935
;         FILING DATE: 14-APR-1994
;   INFORMATION FOR SEQ ID NO: 35:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 9 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;         DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
;         DESCRIPTION: SYNTHETIC DNA"
  PCT-US95-04477-35

Qy        Query Match    100.0%; Score 9; DB 5; Length 9;
Db        Best Local Similarity 100.0%; Pred. No. 1.9e+07;
          Matches  9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy  1 ttctgagaa 9
       |||||||||
Db  9 TTCTGAGAA 1


RESULT 6
PCT-US95-17025-34/c
Sequence 34, Application PC/US9517025
;   GENERAL INFORMATION:
;       APPLICANT: James E. Darnell, Jr.
;       APPLICANT: Zilong Wen
;       APPLICANT: Curt M. Horvath
;       APPLICANT: Zhong Zhong
;       TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
;       TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
;       NUMBER OF SEQUENCES: 39
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Klauber & Jackson
;         STREET: 411 Hackensack Avenue
;         CITY: Hackensack
;         STATE: New Jersey
;         COUNTRY: USA
;         ZIP: 07601
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.25
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 08/369,796
;         FILING DATE: 06-JAN-1995
;         CLASSIFICATION:
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Jackson Esq., David A.
;         REGISTRATION NUMBER: 26,742
;         REFERENCE/DOCKET NUMBER: 600-1-116
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 201 487-5800
;         TELEFAX: 201 343-1684
;         TELEX: 133521
;   INFORMATION FOR SEQ ID NO: 34:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 9 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: double
;         TOPOLOGY: linear
;       MOLECULE TYPE: DNA synthetic probe
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
  PCT-US95-17025-34

Qy        Query Match    100.0%; Score 9; DB 5; Length 9;
Db        Best Local Similarity 100.0%; Pred. No. 1.9e+07;
          Matches  9; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

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Db  9 TTCTGAGAA 1


RESULT 7
US-08-440-787A-85/c
Sequence 85, Application US/0844078TA
Patent No. 5770434
;   GENERAL INFORMATION:
;       APPLICANT: Huse, William D.
;       TITLE OF INVENTION: Soluble Peptides Having Constrained,
;       TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
;       TITLE OF INVENTION: Same.
;       NUMBER OF SEQUENCES: 174
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Campbell & Flores LLP
```

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-440-787A-85

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Qy   2 tctgagaa 9
         ||||||||
Db  10 TCTGAGAA 3
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Query Match   88.9%; Score 8; DB 1; Length 10;
Best Local Similarity   100.0%; Pred. No. 3.6e+03;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 8
US-08-440-787A-86
Sequence 86, Application US/08440787A
Patent No. 5770434
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained,
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
TITLE OF INVENTION: Same.
NUMBER OF SEQUENCES: 174
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-440-787A-86

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Qy   1 ttctgaga 8
         ||||||||
Db   3 TTCTGAGA 10
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Query Match   88.9%; Score 8; DB 1; Length 10;
Best Local Similarity   100.0%; Pred. No. 3.6e+03;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 9
US-08-268-799-3/c
Sequence 3, Application US/08268799
Patent No. 5654195
GENERAL INFORMATION:
APPLICANT: Sodroski, Joseph
APPLICANT: Haseltine, William A.
APPLICANT: Letvin, No. 5654195man
APPLICANT: Li, John
TITLE OF INVENTION: Vectors Expressing Hybrid Viruses,
TITLE OF INVENTION: Methods Of Use And No. 5654195el Assays
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts and Cushman
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887,505
FILING DATE: 22-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41858
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 stre ur
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

US-08-268-799-3

Query Match   82.2%; Score 7.4; DB 1; Length 9;
Best Local Similarity   88.9%; Pred. No. 1.9e+07;

RESULT 10
US-08-411-020-12

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Qy      1  ttctgagaa  9
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Db      9  TTCTGAAAA  1
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Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

; Sequence 12, Application US/08411020
; Patent No. 5712094
; GENERAL INFORMATION:
;   APPLICANT: SEIDEL, H. MARTI
;   APPLICANT: LAMB, I. PETER
;   APPLICANT: CHAN, SHIN-SHAY TIAN
;   TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
;   TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ligand Pharmaceuticals Incorporated
;   STREET: 9393 Towne Centre Drive
;   CITY: San Diego
;   STATE: California
;   COUNTRY: US
;   ZIP: 92121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/411,020
;   FILING DATE: 27-MAR-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jurgensen, Thomas E.
;   REGISTRATION NUMBER: 34,195
;   REFERENCE/DOCKET NUMBER: 016-0030.US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 550-7675
;   TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
;   DESCRIPTION: SYNTHETIC DNA"
US-08-411-020-12
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RESULT 11
US-08-411-020-12/c

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Qy      1  ttctgagaa  9
           |||| ||||
Db      1  TTCTTAGAA  9
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Query Match   82.2%; Score 7.4; DB 1; Length 9;
Best Local Similarity   88.9%; Pred. No. 1.9e+07;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

; Sequence 12, Application US/08411020
; Patent No. 5712094
; GENERAL INFORMATION:
;   APPLICANT: SEIDEL, H. MARTI
;   APPLICANT: LAMB, I. PETER
;   APPLICANT: CHAN, SHIN-SHAY TIAN
;   TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
;   TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
;   NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ligand Pharmaceuticals Incorporated
;   STREET: 9393 Towne Centre Drive
;   CITY: San Diego
;   STATE: California
;   COUNTRY: US
;   ZIP: 92121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/411,020
;   FILING DATE: 27-MAR-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jurgensen, Thomas E.
;   REGISTRATION NUMBER: 34,195
;   REFERENCE/DOCKET NUMBER: 016-0030.US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 550-7675
;   TELEFAX: (619) 535-3906
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
;   DESCRIPTION: SYNTHETIC DNA"
US-08-411-020-12

RESULT 12
US-08-411-020-13
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Qy      1  ttctgagaa  9
           ||||  ||||
Db      9  TTCTTAGAA  1
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Query Match   82.2%; Score 7.4; DB 1; Length 9;
Best Local Similarity   88.9%; Pred. No. 1.9e+07;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

; Sequence 13, Application US/08411020
; Patent No. 5712094
; GENERAL INFORMATION:
;   APPLICANT: SEIDEL, H. MARTI
;   APPLICANT: LAMB, I. PETER
;   APPLICANT: CHAN, SHIN-SHAY TIAN
;   TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR
;   TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION
;   NUMBER OF SEQUENCES: 59
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Ligand Pharmaceuticals Incorporated
;   STREET: 9393 Towne Centre Drive
;   CITY: San Diego
;   STATE: California
;   COUNTRY: US
;   ZIP: 92121
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/411,020
;   FILING DATE: 27-MAR-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jurgensen, Thomas E.

; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0030.US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 550-7675
; TELEFAX: (619) 535-3906
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,
; DESCRIPTION: SYNTHETIC DNA"
; US-08-411-020-13

Qy   82.2%;   Score 7.4; DB 1; Length 9;
Query Match
Best Local Similarity   88.9%;   Pred. No. 1.9e+07;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ttctgagaa 9
         ||||| |||
Db   1 TTCTCAGAA 9

RESULT 13
US-08-369-796-31/c
Sequence 31, Application US/08369796
Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA synthetic probe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-369-796-31

Query Match
Best Local Similarity   88.9%;   Pred. No. 1.9e+07;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;
US-08-369-796-34

Qy   1 ttctgagaa 9
         |||| |||
Db   9 TTCTGGGAA 1

RESULT 14
US-08-369-796-34
Sequence 34, Application US/08369796
Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA synthetic probe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-369-796-34

Query Match   82.2%;   Score 7.4; DB 1; Length 9;
Best Local Similarity   88.9%;   Pred. No. 1.9e+07;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ttctgagaa 9
         ||||| |||
Db   1 TTCTCAGAA 9

RESULT 15
US-08-369-796-36/c
Sequence 36, Application US/08369796
Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.

```
~  APPLICANT:  Zilong Wen
~  APPLICANT:  Curt M. Horvath
~  APPLICANT:  Zhong Zhong
~  TITLE OF INVENTION:  FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
~  TITLE OF INVENTION:  TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
~  NUMBER OF SEQUENCES:  39
~  CORRESPONDENCE ADDRESS:
~   ADDRESSEE:  Klauber & Jackson
~   STREET:  411 Hackensack Avenue
~   CITY:  Hackensack
~   STATE:  New Jersey
~   COUNTRY:  USA
~   ZIP:  07601
~  COMPUTER READABLE FORM:
~   MEDIUM TYPE:  Floppy disk
~   COMPUTER:  IBM PC compatible
~   OPERATING SYSTEM:  PC-DOS/MS-DOS
~   SOFTWARE:  PatentIn Release #1.0, Version #1.25
~  CURRENT APPLICATION DATA:
~   APPLICATION NUMBER:  US/08/369,796
~   FILING DATE:  06-JAN-1995
~   CLASSIFICATION:  435
~  ATTORNEY/AGENT INFORMATION:
~   NAME:  Jackson Esq., David A.
~   REGISTRATION NUMBER:  26,742
~   REFERENCE/DOCKET NUMBER:  600-1-116
~  TELECOMMUNICATION INFORMATION:
~   TELEPHONE:  201 487-5800
~   TELEFAX:  201 343-1684
~   TELEX:  133521
~  INFORMATION FOR SEQ ID NO:  36:
~  SEQUENCE CHARACTERISTICS:
~   LENGTH:  9 base pairs
~   TYPE:  nucleic acid
~   STRANDEDNESS:  double
~   TOPOLOGY:  linear
~   MOLECULE TYPE:  DNA synthetic probe
~   HYPOTHETICAL:  NO
~   ANTI-SENSE:  NO
~  US-08-369-796-36
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Query Match                82.2%;    Score 7.4;   DB 1;     Length 9;
Best Local Similarity      88.9%;    Pred. No. 1.9e+07;
Matches     8;  Conservative    0;  Mismatches  1;  Indels   0;  Gaps   0;

Qy    1  ttctgagaa 9
         ||| ||||||
Db    9  TTCCGAGAA 1
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Search completed: April 21, 2001, 13:12:32
Job time: 3545 sec

OM nucleic - nucleic search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: April 21, 2001, 12:14:34 ; Search time 110.76 Seconds
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                                             47.436 Million cell updates/sec

Title: SHORT
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 65774

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 12

Database :   N_Geneseq_0401:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Match	Query Length	DB Length	ID	Description
1	9	100.0	9	16	T14149	Cytokine responsiv
2	9	100.0	9	17	T14183	Cytokine activated
3	9	100.0	9	19	V56876	Regulatory element
4	8	88.9	8	20	X77642	Nil active EGS 6.
5	7.4	82.2	9	14	Q53424	SIVmac/HIV-1 junct
6	7.4	82.2	9	16	T14165	Cytokine responsiv
7	7.4	82.2	9	16	T14165	Cytokine responsiv
8	7.4	82.2	9	16	T14155	Cytokine responsiv
9	7.4	82.2	9	16	T14145	Cytokine responsiv
10	7.4	82.2	9	17	T41582	Cytokine activated
11	7.4	82.2	9	17	T41582	Cytokine activated
12	7.4	82.2	9	17	T41583	Cytokine activated
13	7.4	82.2	9	19	V56892	Regulatory element
14	7.4	82.2	9	19	V56892	Regulatory element
15	7.4	82.2	9	19	V56876	Regulatory element
16	7.4	82.2	9	19	V56872	Regulatory element
17	7.4	82.2	9	19	V11639	Fc-gamma RI promot
18	7.4	82.2	9	21	C83341	Interleukin-6 resp
19	7.4	82.2	10	16	T14167	Cytokine responsiv
20	7.4	82.2	10	16	T14167	Cytokine responsiv
21	7.4	82.2	10	16	V56894	Regulatory element
22	7.4	82.2	10	19	V56894	Regulatory element
23	7.4	82.2	10	21	Z81339	Metastatic breast
24	7.4	82.2	10	21	Z84449	Metastatic breast
25	7.4	82.2	10	21	Z85845	Metastatic breast
26	7.4	82.2	10	22	Z86651	Metastatic breast
27	7.4	82.2	10	22	F36105	Yeast NORF gene SA
28	7.4	82.2	10	22	F36115	Yeast NORF gene SA
29	7.4	82.2	10	22	F40413	Yeast NORF gene SA
30	7.4	82.2	10	22	F43208	Yeast NORF gene SA
31	7.4	82.2	10	22	F43604	Yeast NORF gene SA
32	7.4	82.2	10	22	F44027	Yeast NORF gene SA
33	7.4	82.2	11	20	Z19018	Murine MRL SAGE ta
34	7.4	82.2	11	20	Z18836	Murine C57BL/6 SAG
35	7.4	82.2	11	20	Z18737	Murine C57BL/6 SAG
36	7.4	77.8	11	20	X25606	Yeast NMD2 mRNA co
37	7.4	77.8	11	22	A39462	Potential ribozyme
38	7.4	77.8	11	21	A81203	A. thaliana primer
39	7	77.8	8	21	A28766	Tethered probe CF1
40	7	77.8	9	15	Q45107	5'-primer #18 for
41	7	77.8	10	18	T66061	(dC-dA)n.(dG-dT)n
42	7	77.8	10	20	X15564	Differential displ
43	7	77.8	10	20	X02705	Barley HPPD primer
44	7	77.8	10	21	C64164	PCR primer AG164,
45	7	77.8	10	21	A56432	Human macrophage 9

ALIGNMENTS

RESULT 1
ID   T14149 standard; DNA; 9 BP.
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AC   T14149;
XX
DT   29-MAY-1996 (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signaling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995; 95WO-US04477.
XX
PR   27-MAR-1995; 95US-0410780.
PR   14-APR-1994; 94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample

```
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signaling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;
XX

Query Match             100.0%;  Score 9;  DB 16;  Length 9;
Best Local Similarity   100.0%;  Pred. No. 6.5e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  ttctgagaa  9
          |||||||||
Db     9  TTCTGAGAA  1


RESULT  2
ID   T41583/c   T41583 standard; DNA;  9 BP.
XX
AC   T41583;
XX
DT   04-JUN-1997  (first entry)
XX
DE   Cytokine activated STAT protein dependent DNA regulatory element.
XX
KW   Regulatory element; protein; cytokine; responsive; host cell;
KW   transfection; agonist; antagonist; mediated; transcription;
KW   modulation; STAT; STAT5; STAT6; signaling pathway; ss.
XX
OS   Synthetic.
XX
PN   WO9630515-A1.
XX
PD   03-OCT-1996.
XX
DR   WPI; 1996-455362/45.
XX
PF   25-MAR-1996;  96WO-US04012.
XX
PR   27-MAR-1995;  95US-0411020.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM, Tian Chan S;
XX
PT   DNA construct for screening modulators of cytokine-mediated
PT   transcription - contg. regulatory element and a cytokine-sensitive
PT   promoter operably linked to a heterologous gene
XX
PS   Claim 5; Page 61; 72pp; English.
XX
CC   A novel DNA construct comprises an oligonucleotide (ON) comprising
CC   a regulatory element having the present sequence, operably linked
CC   to a promoter, which is operably linked to a heterologous gene
CC   (preferably a marker gene). The gene is under the transcriptional
CC   control of the promoter and the ON sequence when the ON is bound by
CC   a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
CC   erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
CC   IL-13 or IL-15. Cytokine responsive host cells transfected with the
CC   DNA construct can be used to measure the ability of a compound to
CC   act as an agonist or antagonist of cytokine mediated gene
CC   transcription. In particular, they can be used to screen for
```

```
CC   cytokine modulators involved in the STAT5 and/or STAT6 protein
CC   signaling pathway.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;
XX

Query Match             100.0%;  Score 9;  DB 17;  Length 9;
Best Local Similarity   100.0%;  Pred. No. 6.5e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  ttctgagaa  9
          |||||||||
Db     9  TTCTGAGAA  1


RESULT  3
ID   V56876/c   V56876 standard; DNA;  9 BP.
XX
AC   V56876;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Regulatory element containing oligonucleotide #35.
XX
KW   Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW   transcriptional control; STAT protein; screening; agonist; ss.
XX
OS   Synthetic.
XX
PN   US5814517-A.
XX
PD   29-SEP-1998.
XX
PF   27-MAR-1995;  95US-0410779.
PR   27-MAR-1995;  95US-0410779.
PR   14-APR-1994;  94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM;
XX
DR   WPI; 1998-541763/46;
XX
PT   DNA constructs containing cytokine-responsive regulatory elements -
PT   useful in assays for transcription-regulating proteins or gene
PT   transcription agonists or antagonists
XX
PS   Disclosure; Column 11; 58pp; English.
XX
CC   V56842-V56976 and V61601-V61631 are oligonucleotides used in the
CC   production of constructs comprising a cytokine-responsive regulatory
CC   element linked to a promoter which is linked to a heterologous coding
CC   sequence so that the coding sequence is under the transcriptional control
CC   of the regulatory element and the promoter, where the regulatory element
CC   has a nucleotide sequence selected from the promoter, TTCNGAA, TTANyTAA, and TTCNyTAA,
CC   where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC   detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC   in a sample by contacting the sample with the construct so that the
CC   protein binds to the regulatory element, and detecting or separating the
CC   resulting complex. The cells can be used in screening assays for agonists
CC   of gene transcription, in which the level of expression of the coding
CC   sequence is measured in the presence and absence of a test compound or
CC   in the presence of the corresponding cytokine.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;
XX

Query Match             100.0%;  Score 9;  DB 19;  Length 9;
Best Local Similarity   100.0%;  Pred. No. 6.5e+07;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

RESULT 4

```
Qy    1 ttctgagaa 9
        |||||||||
Db    9 TTCTGAGAA 1
```

```
ID   X77642/c  X77642 standard; DNA; 11 BP.
XX
AC   X77642;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Nil active EGS 6.
XX
KW   External guide sequence; EGS; target mRNA; identification; diagnostic;
KW   inactivation; essential gene; therapy; ss.
XX
OS   Synthetic.
XX
PN   WO9927135-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998; 98WO-US24854.
XX
PR   20-NOV-1998; 98US-0079851.
PR   30-MAR-1998; 98US-0079851.
PR   21-NOV-1997; 97US-0976220.
XX
PA   (INNO-) INNOVIR LAB INC.
XX
PI   Kindt TJ, Nilsen TW, Robertson HD;
XX
DR   WPI; 1999-357853/30.
XX
PT   Identifying and inhibiting functional nucleic acid molecules in
PT   cells
XX
PS   Example 3; Page 28; 58pp; English.
XX
CC   This invention describes a novel method allowing essential or functional
CC   genes to be rapidly identified and inactivated. The method is able to
CC   firstly identify most of the essential genes in an organism (i.e. a
CC   bacteria or a eukaryote) needed for survival, and secondly it provides
CC   for reducing or inactivating their expression. The method is able to
CC   identify functional oligonucleotide molecules able to be used as
CC   diagnostic reagents and therapeutics. The method provides a means for
CC   identifying essential genes whose sequence is known only as part of a
CC   genome with unknown function, as well as a means for identifying
CC   functional oligonucleotide molecules. The method involves the use of a
CC   nucleic acid molecule comprising (a) a first reporter gene encoding a
CC   fusion protein comprising a protein of interest (itself translated from
CC   an RNA of interest) and a reporter protein, and (b) a second reporter gene
CC   encoding a second reporter protein, and (c) a targeting gene encoding a
CC   functional oligonucleotide molecule such as an external guide sequence
CC   (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest
CC   at a site on the first reporter gene able to encode the RNA of interest.
XX
SQ   Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 other;
```

```
Query Match             88.9%;  Score 8;  DB 20;  Length 11;
Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
```

RESULT 5

```
Qy    1 ttctgaga 8
        ||||||||
Db    9 TTCTGAGA 2
```

```
ID   Q53424/c  Q53424 standard; DNA; 9 BP.
XX
AC   Q53424;
XX
DT   16-JUN-1994  (first entry)
XX
DE   SIVmac/HIV-1 junction region #3.
XX
KW   Junction fragment; vector; simian immunodeficiency virus; SIV; gag;
KW   pol; vif; vpx; long terminal repeat; LTR; HIV-1; env; tat; rev;
KW   nef; vpr; chimeric virus; replication competent; monkey; mandril;
KW   macaque; disease progression; vaccine; epitope; immune response;
KW   envelope glycoprotein; cytotoxic T lymphocyte; ss.
XX
OS   Synthetic.
XX
PN   WO9324632-A.
XX
PD   09-DEC-1993.
XX
PF   22-MAY-1992; 92US-0887505.
XX
PR   20-MAY-1993; 93WO-US04814.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Haseltine WA, Letvin N, Li J, Sodroski J;
XX
DR   WPI; 1993-405823/50.
XX
PT   Hybrid SIV-HIV-1 viral vectors - used to provide animal models
PT   for HIV-1 infection or a therapeutic agents or in vaccines for
PT   HIV-1
XX
PS   Disclosure; Fig 1C; 72pp; English.
XX
CC   The sequences given in Q53422-28 represent junction fragments which
CC   were used in the construction the vectors of the invention. These
CC   vectors contain a 5' DNA segment which contains a sufficient number
CC   of nucleotides corresponding to a functional gag, pol, vif and vpx
CC   protein and has a SIV long terminal repeat (LTR), and a 3' DNA segment which contains
CC   a sufficient number of nucleotides corresponding to at least one
CC   HIV-1 genome to encode a functional HIV-1 env, tat and rev protein
CC   and a sufficient number of nucleotides corresponding to a SIV genome
CC   to encode a functional nef protein and has a SIV LTR. The vector
CC   further comprises a sufficient number of nucleotides corresponding to
CC   the SIV genome to encode a functional SIV vpr protein. Vectors such
CC   as these produce chimeric viruses containing HIV-1 components. As a
CC   result of transfecting cells with these vectors, replication competent
CC   viruses that are infectious in animal systems such as monkeys, eg.
CC   mandrils, macaques, etc. can be produced. The vectors can be used for
CC   creating an animal model for studying disease progression by HIV-1,
CC   for screening for compounds exhibiting anti-HIV activity, for screening
CC   for a vaccine aginst HIV infection and for determining the specific
CC   epitopes of a HIV-1 envelope glycoprotein recognised by cytotoxic T
CC   lymphocytes. They can also be used to boost immune response in a HIV
CC   infected individual or as a vaccine to prevent infection.
XX
SQ   Sequence 9 BP; 3 A; 1 C; 1 G; 4 T; 0 other;
```

```
Query Match             82.2%;  Score 7.4;  DB 14;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 6.5e+07;
Matches    8;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
```

RESULT 6
T14165

```
Qy    1 ttctgagaa 9
        ||||| |||
Db    9 TTCTGAAAA 1
```

```
ID   T14165 standard; DNA; 9 BP.
XX
AC   T14165;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;  95WO-US04477.
XX
PR   27-MAR-1995;  95US-0410780.
PR   14-APR-1994;  94US-0228935.
XX
PI   Lamb IP, Seidel HM;
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample.
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match             82.2%;  Score 7.4;  DB 16;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 6.5e+07;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ttctgagaa 9
              |||| ||||
Db          1 tcttaagaa 9

RESULT   7
ID   T14165/c
ID   T14165 standard; DNA; 9 BP.
XX
AC   T14165;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
```

```
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;  95WO-US04477.
XX
PR   27-MAR-1995;  95US-0410780.
PR   14-APR-1994;  94US-0228935.
XX
PI   Lamb IP, Seidel HM;
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol. i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match             82.2%;  Score 7.4;  DB 16;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 6.5e+07;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ttctgagaa 9
              |||| ||||
Db          9 TTCTTAGAA 1

RESULT   8
ID   T14149
ID   T14149 standard; DNA; 9 BP.
XX
AC   T14149;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;  95WO-US04477.
XX
PR   27-MAR-1995;  95US-0410780.
PR   14-APR-1994;  94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM;
```

```
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   Tr(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match     82.2%;  Score 7.4;  DB 16;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 6.5e+07;
Matches    8;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 ttctgagaa 9
        ||||| |||
Db    1 ttctcagaa 9


RESULT   9
ID   T14145/c
     T14145 standard; DNA; 9 BP.
XX
AC   T14145;
XX
DT   29-MAY-1996  (first entry)
XX
DE   Cytokine responsive DNA spacer regulatory element.
XX
KW   Regulatory element; transcriptional regulatory protein;
KW   signaling molecule; DNA spacer; agonist; antagonist; anaemia;
KW   gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9528482-A2.
XX
PD   26-OCT-1995.
XX
PF   10-APR-1995;  95WO-US04477.
XX
PR   27-MAR-1995;  95US-0410780.
PR   14-APR-1994;  94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM;
XX
DR   WPI; 1995-373797/48.
XX
PT   DNA spacer regulatory elements responsive to cytokine(s) - for
PT   detecting the presence of transcriptional regulatory protein in a
PT   sample
XX
PS   Claim 7; Page 125; 135pp; English.
XX
CC   The present oligonucleotide comprises a regulatory element
CC   Tr(Nx)AA, where x is 4-7, and the regulatory element binds an
CC   activated transcriptional regulatory protein in response to a
CC   signalling mol., i.e. a cytokine. This cytokine responsive DNA
```

```
CC   spacer regulatory element can be used to detect the presence of
CC   a transcriptional regulatory protein in a sample, and in assays
CC   for (ant)agonists of gene transcription. The identified cpds.
CC   may be used to treat cytokine-induced disease states, or to
CC   ameliorate disease states caused by cytokine deficiency, e.g.
CC   inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ   Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;

Query Match     82.2%;  Score 7.4;  DB 16;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 6.5e+07;
Matches    8;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 ttctgagaa 9
        ||||| |||
Db    9 TTCTGGGAA 1


RESULT   10
ID   T41582
     T41582 standard; DNA; 9 BP.
XX
AC   T41582;
XX
DT   04-JUN-1997  (first entry)
XX
DE   Cytokine activated STAT protein dependent DNA regulatory element.
XX
KW   Regulatory element; protein; cytokine; responsive; host cell;
KW   transfection; agonist; antagonist; mediated; transcription;
KW   modulation; STAT; STAT5; STAT6; signalling pathway; ss.
XX
OS   Synthetic.
XX
PN   WO9630515-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;  96WO-US04012.
XX
PR   27-MAR-1995;  95US-0411020.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP,  Seidel HM,  Tian Chan S;
XX
DR   WPI; 1996-455362/45.
XX
PT   DNA construct for screening modulators of cytokine-mediated
PT   transcription  - contg. regulatory element and a cytokine-sensitive
PT   promoter operably linked to a heterologous gene
XX
PS   Claim 5; Page 61; 72pp; English.
XX
CC   A novel DNA construct comprises an oligonucleotide (ON) comprising
CC   a regulatory element having the present sequence, operably linked
CC   to a promoter, which is operably linked to a heterologous gene
CC   (preferably a marker gene). The gene is under the transcriptional
CC   control of the promoter and the ON sequence when the ON is bound by
CC   a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
CC   erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
CC   IL-13 or IL-15. Cytokine responsive host cells transfected with the
CC   DNA construct can be used to measure the ability of a compound to
CC   act as an agonist or antagonist of cytokine mediated gene
CC   transcription. In particular, they can be used to screen for
CC   cytokine modulators involved in the STAT5 and/or STAT6 protein
CC   signalling pathway.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match     82.2%;  Score 7.4;  DB 17;  Length 9;
```

```
Qy    1 ttctgagaa 9
        ||||| ||||
Db    1 ttctaagaa 9

Best Local Similarity   88.9%;
Matches    8;  Conservative   0;  Pred. No. 6.5e+07;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 11
T41582/c
ID   T41582 standard; DNA; 9 BP.
XX
AC   T41582;
XX
DT   04-JUN-1997  (first entry)
XX
DE   Cytokine activated STAT protein dependent DNA regulatory element.
XX
KW   Regulatory element; protein; cytokine; responsive; host cell;
KW   transfection; agonist; antagonist; mediated; transcription;
KW   modulation; STAT; STAT5; STAT6; signalling pathway; ss.
XX
OS   Synthetic.
XX
PN   WO9630515-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;  96WO-US04012.
XX
PR   27-MAR-1995;  95US-0411020.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM, Tian Chan S;
XX
DR   WPI; 1996-455362/45.
XX
PT   DNA construct for screening modulators of cytokine-mediated
PT   transcription - contg. regulatory element and a cytokine-sensitive
PT   promoter operably linked to a heterologous gene
XX
PS   Claim 5; Page 61; 72pp; English.
XX
CC   A novel DNA construct comprises an oligonucleotide (ON) comprising
CC   a regulatory element having the present sequence, operably linked
CC   to a promoter, which is operably linked to a heterologous gene
CC   (preferably a marker gene). The gene is under the transcriptional
CC   control of the promoter and the ON sequence when the ON is bound by
CC   a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
CC   erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
CC   IL-13 or IL-15. Cytokine responsive host cells transfected with the
CC   DNA construct can be used to measure the ability of a compound to
CC   act as an agonist or antagonist of cytokine mediated gene
CC   transcription. In particular, they can be used to screen for
CC   cytokine modulators involved in the STAT5 and/or STAT6 protein
CC   signalling pathway.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match             82.2%;  Score 7.4;  DB 17;  Length 9;
Best Local Similarity   88.9%;
Matches    8;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 ttctgagaa 9
        ||||| ||||
Db    9 TTCTTAGAA 1

RESULT 12
ID   T41583 standard; DNA; 9 BP.
```

```
Qy    1 ttctgagaa 9
        ||||| ||||
Db    1 ttctaagaa 9

Best Local Similarity   88.9%;
Matches    8;  Conservative   0;  Pred. No. 6.5e+07;  Mismatches  1;  Indels  0;  Gaps  0;

XX
AC   T41583;
XX
DT   04-JUN-1997  (first entry)
XX
DE   Cytokine activated STAT protein dependent DNA regulatory element.
XX
KW   Regulatory element; protein; cytokine; responsive; host cell;
KW   transfection; agonist; antagonist; mediated; transcription;
KW   modulation; STAT; STAT5; STAT6; signalling pathway; ss.
XX
OS   Synthetic.
XX
PN   WO9630515-A1.
XX
PD   03-OCT-1996.
XX
PF   25-MAR-1996;  96WO-US04012.
XX
PR   27-MAR-1995;  95US-0411020.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM, Tian Chan S;
XX
DR   WPI; 1996-455362/45.
XX
PT   DNA construct for screening modulators of cytokine-mediated
PT   transcription - contg. regulatory element and a cytokine-sensitive
PT   promoter operably linked to a heterologous gene
XX
PS   Claim 5; Page 61; 72pp; English.
XX
CC   A novel DNA construct comprises an oligonucleotide (ON) comprising
CC   a regulatory element having the present sequence, operably linked
CC   to a promoter, which is operably linked to a heterologous gene
CC   (preferably a marker gene). The gene is under the transcriptional
CC   control of the promoter and the ON sequence when the ON is bound by
CC   a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,
CC   erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,
CC   IL-13 or IL-15. Cytokine responsive host cells transfected with the
CC   DNA construct can be used to measure the ability of a compound to
CC   act as an agonist or antagonist of cytokine mediated gene
CC   transcription. In particular, they can be used to screen for
CC   cytokine modulators involved in the STAT5 and/or STAT6 protein
CC   signalling pathway.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match             82.2%;  Score 7.4;  DB 17;  Length 9;
Best Local Similarity   88.9%;
Matches    8;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 ttctgagaa 9
        ||||| ||||
Db    1 ttctcagaa 9

RESULT 13
V56892
ID   V56892 standard; DNA; 9 BP.
XX
AC   V56892;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Regulatory element containing oligonucleotide #51.
XX
KW   Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW   transcriptional control; STAT protein; screening; agonist; ss.
XX
OS   Synthetic.
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RESULT 14

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ID   V56892 standard; DNA; 9 BP.
V56892/c
XX
AC   V56892;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Regulatory element containing oligonucleotide #51.
XX
KW   Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW   transcriptional control; STAT protein; screening; agonist; ss.
XX
OS   Synthetic.
XX
PN   US5814517-A.
XX
PD   29-SEP-1998.
XX
PF   27-MAR-1995;   95US-0410779.
XX
PR   27-MAR-1995;   95US-0410779.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM;
XX
DR   WPI; 1998-541763/46.
XX
PT   DNA constructs containing cytokine-responsive regulatory elements -
PT   useful in assays for transcription-regulating proteins or gene
PT   transcription agonists or antagonists
XX
PS   Disclosure; Column 12; 58pp; English.
XX
CC   V56842-V55976 and V61601-V61631 are oligonucleotides used in the
CC   production of constructs comprising a cytokine-responsive regulatory
CC   element linked to a promoter which is linked to a heterologous coding
CC   sequence so that the coding sequence is under the transcriptional control
CC   of the regulatory element and the promoter, where the regulatory element
CC   has a nucleotide sequence selected from TTCNNGAA, TTANyTAA, and TTCNyTAA
CC   where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC   detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC   in a sample by contacting the sample with the construct so that the
CC   protein binds to the regulatory element, and detecting or separating the
CC   resulting complex. The cells can be used in screening assays for agonists
CC   of gene transcription, in which the level of expression of the coding
CC   sequence is measured in the presence and absence of a test compound or
CC   in the presence of the corresponding cytokine.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;
XX
XX

Query Match    82.2%;   Score 7.4;  DB 19;   Length 9;
Best Local Similarity   88.9%;   Pred. No. 6.5e+07;
Matches   8;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 ttctgagaa 9
       ||||  ||||
Db   1 ttctaagaa 9
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RESULT 15

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ID   V56876 standard; DNA; 9 BP.
V56876
XX
AC   V56876;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Regulatory element containing oligonucleotide #35.
XX
KW   Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW   transcriptional control; STAT protein; screening; agonist; ss.
XX
OS   Synthetic.
XX
PN   US5814517-A.
XX
PD   29-SEP-1998.
XX
PF   27-MAR-1995;   95US-0410779.
XX
PR   27-MAR-1995;   95US-0410779.
PR   14-APR-1994;   94US-0228935.
XX
PA   (LIGA-) LIGAND PHARM INC.
XX
PI   Lamb IP, Seidel HM;
XX
DR   WPI; 1998-541763/46.
XX
PT   DNA constructs containing cytokine-responsive regulatory elements -
PT   useful in assays for transcription-regulating proteins or gene
PT   transcription agonists or antagonists
XX
PS   Disclosure; Column 12; 58pp; English.
XX
CC   V56842-V55976 and V61601-V61631 are oligonucleotides used in the
CC   production of constructs comprising a cytokine-responsive regulatory
CC   element linked to a promoter which is linked to a heterologous coding
CC   sequence so that the coding sequence is under the transcriptional control
CC   of the regulatory element and the promoter, where the regulatory element
CC   has a nucleotide sequence selected from TTCNNGAA, TTANyTAA, and TTCNyTAA
CC   where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC   detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC   in a sample by contacting the sample with the construct so that the
CC   protein binds to the regulatory element, and detecting or separating the
CC   resulting complex. The cells can be used in screening assays for agonists
CC   of gene transcription, in which the level of expression of the coding
CC   sequence is measured in the presence and absence of a test compound or
CC   in the presence of the corresponding cytokine.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;
XX
XX

Query Match    82.2%;   Score 7.4;  DB 19;   Length 9;
Best Local Similarity   88.9%;   Pred. No. 6.5e+07;
Matches   8;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 ttctgagaa 9
       ||||  ||||
Db   9 TTCTTAGAA 1
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PS   Disclosure; Column 11; 58pp; English.
XX
CC   V56842-V56976 and V61601-V61631 are oligonucleotides used in the
CC   production of constructs comprising a cytokine-responsive regulatory
CC   element linked to a promoter which is linked to a heterologous coding
CC   sequence so that the coding sequence is under the transcriptional control
CC   of the regulatory element and the promoter, where the regulatory element
CC   has a nucleotide sequence selected from TTCNNGAA, TTANyTAA, and TTCNyTAA
CC   where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC   detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC   in a sample by contacting the sample with the construct so that the
CC   protein binds to the regulatory element, and detecting or separating the
CC   resulting complex. The cells can be used in screening assays for agonists
CC   of gene transcription, in which the level of expression of the coding
CC   sequence is measured in the presence and absence of a test compound or
CC   in the presence of the corresponding cytokine.
XX
SQ   Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match   82.2%;   Score 7.4;   DB 19;   Length 9;
Best Local Similarity   88.9%;   Pred. No. 6.5e+07;
Matches   8;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 ttctgagaa 9
          ||| ||||
Db   1 ttctcagaa 9

Search completed: April 21, 2001, 13:14:35
Job time: 3601 sec

OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: April 21, 2001, 11:42:58 ; Search time 1240.49 Seconds
                                             (without alignments)
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Title: SHORT
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 307896235 6 residues

Total number of hits satisfying chosen parameters: 15938

Post-processing: Minimum Match 0%
Maximum DB seq length: 0
Minimum DB seq length: 12
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*

1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	7.4	82.2	9	9	AX041991	AX041991 Sequence
c 2	7.4	82.2	10	9	AR043683	AR043683 Sequence
c 3	7.4	82.2	10	9	AR043683	AR043683 Sequence
c 4	7.4	82.2	11	9	AR097294	AR097294 Sequence
c 5	7.4	82.2	11	9	AX063656	AX063653 Sequence
c 6	7.4	82.2	11	9	AX063656	AX063656 Sequence
c 7	7.4	82.2	11	10	I39722	I39722 Sequence 9
c 8	7.4	82.2	11	93	I55839	I55839 Sequence 9
c 9	7.4	82.2	12	93	S75371	S75371 beta-hexosa
c 10	7.4	82.2	12	93	S75371	S75371 beta-hexosa
c 11	7	77.8	8	9	AR101594	AR101594 Sequence

RESULT 1

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AX041991/c
LOCUS          AX041991      9 bp    DNA          PAT    23-NOV-2000
DEFINITION     Sequence 21 from Patent WO0065067.
ACCESSION      AX041991
VERSION        AX041991.1    GI:11340754
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 9)
AUTHORS        Nelson,P.S., Hood,L. and Lin,B.
TITLE          Prostate-specific polynucleotides, polypeptides and their methods
               of use
JOURNAL        Patent: WO 0065067-A 21 02-NOV-2000;
               The University of Washington (US)
FEATURES       Location/Qualifiers
source         1..9
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
protein_bind   3 a    3 c    1 g    2 t
               /bound_moiety="Interleukin response element binding site"
BASE COUNT
ORIGIN

Query Match    82.2%;   Score 7.4;  DB 9;  Length 9;
Best Local Similarity   88.9%;  Pred. No. 1.6e+09;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1  ttctgagaa  9
        ||||| |||
Db   9  TTCTGGGAA  1
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ALIGNMENTS

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c  12   7    77.8   10   9   A41392   A41392 Sequence 18
c  13   7    77.8   11   9   A24764   A24764 oligonucleo
c  14   7    77.8   11   9   AR074369 AR074369 Sequence
c  15   7    77.8   12   9   A06058   A06058 Synthetic P
c  16   7    77.8   12   9   A06059   A06059 Synthetic P
c  17   7    77.8   12   9   A16601   A16601 Nucleotide
c  18   7    77.8   12   9   A16602   A16602 Nucleotide
c  19   7    77.8   12   10  I07904   I07904 Sequence 13
c  20   7    77.8   12   10  I07922   I07922 Sequence 34
c  21   6.6  73.3   12   9   A01725   A01725 Vector DNA
c  22   6.6  73.3   12   9   A01735   A01735 Vector DNA
c  23   6.4  71.1   8    9   AR101591 AR101591 Sequence
c  24   6.4  71.1   10   10  E17310   E17310 PCR primer
c  25   6.4  71.1   11   9   A62062   A62062 Sequence 48
c  26   6.4  71.1   12   9   A71450   A71450 Sequence 9
c  27   6.4  71.1   12   9   A87963   A87963 Sequence 11
c  28   6.4  71.1   12   9   A89930   A89930 Sequence 11
c  29   6.4  71.1   12   9   AX059219 AX059219 Sequence
c  30   6.4  71.1   12   10  I39779   I39779 Sequence 52
c  31   6.4  71.1   12   10  AR101242 AR101242 Sequence
c  32   6    66.7   8    9   AR101244 AR101244 Sequence
c  33   6    66.7   8    9   AR101294 AR101294 Sequence
c  34   6    66.7   8    9   AR101393 AR101393 Sequence
c  35   6    66.7   8    9   AR101394 AR101394 Sequence
c  36   6    66.7   8    9   AR101395 AR101395 Sequence
c  37   6    66.7   8    9   AR101540 AR101540 Sequence
c  38   6    66.7   8    9   AR101582 AR101582 Sequence
c  39   6    66.7   8    9   AR101590 AR101590 Sequence
c  40   6    66.7   9    93  S75375   S75375 beta-hexosa
c  41   6    66.7   9    9   AR042901 AR042901 Sequence
c  42   6    66.7   10   10  I22208   I22208 Sequence 22
c  43   6    66.7   10   10  I75076   I75076 Sequence 6
c  44   6    66.7   10   59  S77264   S77264 (3' terminu
c  45   6    66.7
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RESULT 2

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AR043683
LOCUS          AR043683      10 bp   DNA          PAT    29-SEP-1999
DEFINITION     Sequence 53 from patent US 5814517.
ACCESSION      AR043683
VERSION        AR043683.1    GI:5964691
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
               Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Seidel,H.Martin and Lamb,I.Peter.
TITLE          DNA spacer regulatory elements responsive to cytokines and methods
               for their use
JOURNAL        Patent: US 5814517-A 53 29-SEP-1998;
FEATURES       Location/Qualifiers
source         1..10
               /organism="unknown"
BASE COUNT     4 a    1 c    1 g    4 t
ORIGIN

Query Match    82.2%;   Score 7.4;  DB 9;  Length 10;
Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1  ttctgagaa  9
        |||| ||||
Db   2  TTCTAAGAA  10
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RESULT 3

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AR043683/c
LOCUS          AR043683      10 bp   DNA          PAT    29-SEP-1999
DEFINITION     Sequence 53 from patent US 5814517.
ACCESSION      AR043683
VERSION        AR043683.1    GI:5964691
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
               Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Seidel,H.Martin and Lamb,I.Peter.
TITLE          DNA spacer regulatory elements responsive to cytokines and methods
               for their use
JOURNAL        Patent: US 5814517-A 53 29-SEP-1998;
FEATURES       Location/Qualifiers
source         1..10
               /organism="unknown"
BASE COUNT     4 a    1 c    1 g    4 t
ORIGIN

Query Match    82.2%;   Score 7.4;  DB 9;  Length 10;
Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1  ttctgagaa  9
        |||| ||||
Db  10  TTCTAAGAA  2
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RESULT 4

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AR097294
LOCUS          AR097294      11 bp   DNA          PAT    14-FEB-2001
DEFINITION     Sequence 17 from patent US 6071700.
ACCESSION      AR097294
VERSION        AR097294.1    GI:12806024
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
               Unknown.

Query Match    82.2%;   Score 7.4;  DB 9;  Length 10;
Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
Matches  8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   1  ttctgagaa  9
        |||| ||||
Db  10 TTCTTAGAA  2
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                Unclassified.
REFERENCE   1 (bases 1 to 11)
  AUTHORS   He,F. and Jacobson,A.S.
  TITLE     Heterologous polypeptide production in the absence of
            nonsense-mediated mRNA decay functions
  JOURNAL   Patent: US 6071700-A 17 06-JUN-2000;
FEATURES             Location/Qualifiers
  source    1..11
            /organism="unknown"
BASE COUNT  3 a    2 c    2 g    4 t
ORIGIN

Qy    1 ttctgagaa 9
         || ||||||
Db    2 TTTTGAGA 10

Query Match       82.2%;  Score 7.4; DB 9;  Length 11;
Best Local Similarity  88.9%;  Pred. No. 1.1e+06;
Matches    8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 5
LOCUS       AX063653    11 bp    DNA                 PAT       24-JAN-2001
DEFINITION  Sequence 37 from Patent WO0100817.
ACCESSION   AX063653
VERSION     AX063653.1  GI:12541377
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 11)
  AUTHORS   Morgan,A.R. and Severini,A.
  TITLE     Compositions and methods for determining the activity of
            dna-binding proteins and of initiation of transcription
  JOURNAL   Patent: WO 0100817-A 37 04-JAN-2001;
            DNAB Diagnostics, Inc. (CA)
FEATURES             Location/Qualifiers
  source    1..11
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic"
BASE COUNT  2 a    1 c    3 g    5 t
ORIGIN

Qy    1 ttctgagaa 9
         || |||||
Db    1 TTCTGGGAA 9

Query Match       82.2%;  Score 7.4; DB 9;  Length 11;
Best Local Similarity  88.9%;  Pred. No. 1.1e+06;
Matches    8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 6
LOCUS       AX063656/c    11 bp    DNA               PAT       24-JAN-2001
DEFINITION  Sequence 40 from Patent WO0100817.
ACCESSION   AX063656
VERSION     AX063656.1  GI:12541380
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 11)
  AUTHORS   Morgan,A.R. and Severini,A.
  TITLE     Compositions and methods for determining the activity of
            dna-binding proteins and of initiation of transcription
  JOURNAL   Patent: WO 0100817-A 40 04-JAN-2001;
            DNAB Diagnostics, Inc. (CA)
FEATURES             Location/Qualifiers
  source    1..11
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /note="Synthetic"
BASE COUNT  4 a    3 c    1 g    3 t
ORIGIN

Qy    1 ttctgagaa 9
         || |||||
Db   10 TTCTGGGAA 2

Query Match       82.2%;  Score 7.4; DB 9;  Length 11;
Best Local Similarity  88.9%;  Pred. No. 1.1e+06;
Matches    8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 7
LOCUS       I39722    11 bp    DNA                   PAT       13-MAY-1997
DEFINITION  Sequence 9 from patent US 5616489.
ACCESSION   I39722
VERSION     I39722.1  GI:2084202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 11)
  AUTHORS   Levy,D.E.
  TITLE     DNA sequence which binds transcriptional regulatory proteins
            activated in response to various cytokines and uses thereof
  JOURNAL   Patent: US 5616489-A 9 01-APR-1997;
FEATURES             Location/Qualifiers
  source    1..11
            /organism="unknown"
BASE COUNT  3 a    1 c    3 g    4 t
ORIGIN

Qy    1 ttctgagaa 9
         ||||| |||
Db    2 TTCTGGGAA 10

Query Match       82.2%;  Score 7.4; DB 10; Length 11;
Best Local Similarity  88.9%;  Pred. No. 1.1e+06;
Matches    8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

RESULT 8
LOCUS       I55839    11 bp    DNA                   PAT       07-OCT-1997
DEFINITION  Sequence 9 from patent US 5648217.
ACCESSION   I55839
VERSION     I55839.1  GI:2476653
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 11)
  AUTHORS   Levy,D.E.
  TITLE     DNA sequence which binds transcriptional regulatory proteins
            activated in response to various cytokines and uses thereof
  JOURNAL   Patent: US 5648217-A 9 15-JUL-1997;
FEATURES             Location/Qualifiers
  source    1..11
            /organism="unknown"
BASE COUNT  3 a    1 c    3 g    4 t
ORIGIN
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Qy 1 tctgagaa 9
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Db 2 TTCTGGGAA 10

RESULT 9
LOCUS   S75371   12 bp   mRNA   PRI   07-MAY-1993
DEFINITION   S75371 beta-hexosaminidase A (exon 8) [human, mRNA Partial Mutant, 12 nt].
ACCESSION   S75371
VERSION   S75371.1 GI:241964
KEYWORDS   .
SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 12)
  AUTHORS   Akli,S., Chelly,J., Lacorte,J.M., Poenaru,L. and Kahn,A.
  TITLE   Seven novel Tay-Sachs mutations detected by chemical mismatch
             cleavage of PCR-amplified cDNA fragments
  JOURNAL   Genomics 11 (1), 124-134 (1991)
  MEDLINE   9212203
  REMARK   GenBank staff at the National Library of Medicine created this
             entry [NCBI gibbsq 75371] from the original journal article.
             This sequence comes from Figure 4.D.
FEATURES   Location/Qualifiers
     source   1..12
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                     /db_xref="taxon:9606"
     gene   1..12
                     /partial
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BASE COUNT   5 a   2 c   1 g   4 t
ORIGIN

Query Match   82.2%; Score 7.4; DB 93; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.1e+06;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy 1 tctgagaa 9
     |||| |||
Db 4 TTCTTAGAA 12

RESULT 10
LOCUS   S75371/c   12 bp   mRNA   PRI   07-MAY-1993
DEFINITION   S75371 beta-hexosaminidase A (exon 8) [human, mRNA Partial Mutant, 12 nt].
ACCESSION   S75371
VERSION   S75371.1 GI:241964
KEYWORDS   .
SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 12)
  AUTHORS   Akli,S., Chelly,J., Lacorte,J.M., Poenaru,L. and Kahn,A.
  TITLE   Seven novel Tay-Sachs mutations detected by chemical mismatch
             cleavage of PCR-amplified cDNA fragments
  JOURNAL   Genomics 11 (1), 124-134 (1991)
  MEDLINE   9212203
  REMARK   GenBank staff at the National Library of Medicine created this
             entry [NCBI gibbsq 75371] from the original journal article.
             This sequence comes from Figure 4.D.
FEATURES   Location/Qualifiers
     source   1..12
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene   1..12
                     /partial
                     /gene="beta-hexosaminidase A"

BASE COUNT   5 a   2 c   1 g   4 t
ORIGIN

Query Match   82.2%; Score 7.4; DB 93; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.1e+06;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy 1 tctgagaa 9
     |||||| |||
Db 12 TTCTAAGAA 4

RESULT 11
LOCUS   AR101594   8 bp   DNA   PAT   14-FEB-2001
DEFINITION   Sequence 516 from patent US 6083695.
ACCESSION   AR101594
VERSION   AR101594.1 GI:12812392
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 8)
  AUTHORS   Hardin,S.Houck, Homayouni,R. and Hardin,P.Eric.
  TITLE   Optimized primer library for gene sequencing and method of using
             same
  JOURNAL   Patent: US 6083695-A 516 04-JUL-2000;
FEATURES   Location/Qualifiers
     source   1..8
                     /organism="unknown"
BASE COUNT   2 a   2 c   2 g   2 t
ORIGIN

Query Match   77.8%; Score 7; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 2 tctgaga 8
     |||||||
Db 1 TCTGAGA 7

RESULT 12
LOCUS   A41392/c   10 bp   DNA   PAT   05-MAR-1997
DEFINITION   Sequence 18 from Patent WO9426928.
ACCESSION   A41392
VERSION   A41392.1 GI:2297111
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequence.
REFERENCE   1 (bases 1 to 10)
  AUTHORS   Strauss,M. and Bauer,D.
  TITLE   COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
             DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
  JOURNAL   Patent: WO 9426928-A 18 24-NOV-1994;
COMMENT   MAX PLANCK GESELLSCHAFT (DE)
             Other publication DE 4317414 940421.
FEATURES   Location/Qualifiers
     source   1..10
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT   3 a   3 c   2 g   2 t
ORIGIN

Query Match   77.8%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+06;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
RESULT 13
Qy      2 tctgaga 8
          ||||||||
Db      9 TCTGAGA 3

RESULT 13
LOCUS         A24764            11 bp    DNA
A24764/c
DEFINITION    Oligonucleotide PS39.
ACCESSION     A24764
VERSION       A24764.1    GI:833668
KEYWORDS      .
SOURCE        synthetic construct.
  ORGANISM    synthetic construct
              artificial sequence.
REFERENCE     1  (bases 1 to 11)
  AUTHORS
  TITLE       MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS
  JOURNAL     Patent: WO 9309218-A 4 13-MAY-1993;
FEATURES             Location/Qualifiers
  source       1..11
               /organism="synthetic construct"
               /db_xref="taxon:32630"
BASE COUNT      3 a      3 c      2 g      3 t
ORIGIN

Qy      3 ctgagaa 9
          |||||||
Db     11 CTGAGAA 5

Query Match      77.8%;    Score 7;   DB 9;   Length 11;
Best Local Similarity  100.0%;  Pred. No. 2.3e+06;
Matches     7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 14
AR074369/c
LOCUS         AR074369          11 bp    DNA             PAT    28-AUG-2000
DEFINITION    Sequence 4 from patent US 5952547.
ACCESSION     AR074369
VERSION       AR074369.1   GI:10001124
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 11)
  AUTHORS     Cornelissen,M., Soetaert,P., Stam,M., Dockx,J. and Van Aarssen,R.
  TITLE       Modified Bacillus thuringiensis genes with improved expression in
              plant cells, methods of production on and use
  JOURNAL     Patent: US 5952547-A 14-SEP-1999;
FEATURES             Location/Qualifiers
  source       1..11
               /organism="unknown"
BASE COUNT      3 a      3 c      2 g      3 t
ORIGIN

Qy      3 ctgagaa 9
          |||||||
Db     11 CTGAGAA 5

Query Match      77.8%;    Score 7;   DB 9;   Length 11;
Best Local Similarity  100.0%;  Pred. No. 2.3e+06;
Matches     7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 15
A06058
LOCUS         A06058            12 bp    DNA             PAT    25-MAY-1993
DEFINITION    Synthetic primer 476-487.
ACCESSION     A06058
VERSION       A06058.1   GI:411190
```

```
KEYWORDS      synthetic construct.
SOURCE        synthetic construct
  ORGANISM    artificial sequence.
REFERENCE     1  (bases 1 to 12)
  AUTHORS     Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.
  TITLE       Molecular cloning and characterization of the gene sequence coding
              for porcine relaxin
  JOURNAL     Patent: EP 0086649-A 8 24-AUG-1983;
              HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE
FEATURES             Location/Qualifiers
  source       1..12
               /organism="synthetic construct"
               /db_xref="taxon:32630"
BASE COUNT      2 a      2 c      5 g      3 t
ORIGIN

Qy      2 tctgaga 8
          ||||||||
Db      3 TCTGAGA 9

Query Match      77.8%;    Score 7;   DB 9;   Length 12;
Best Local Similarity  100.0%;  Pred. No. 2.3e+06;
Matches     7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Search completed: April 21, 2001, 13:07:39
Job time: 5081 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2001, 11:14:44 ; Search time 1100.03 Seconds
(without alignments)
1.196 Million cell updates/sec

Title: SHORT
Perfect score: 9
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 308

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

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  2: gb_est2:*           45: em_esthum11:*
  3: gb_est3:*           46: em_esthum12:*
  4: gb_est4:*           47: em_esthum13:*
  5: gb_est5:*           48: em_esthum14:*
  6: gb_est6:*           49: em_esthum15:*
  7: gb_est7:*           50: em_esthum16:*
  8: gb_est8:*           51: em_esthum17:*
  9: gb_est9:*           52: em_esthum18:*
 10: gb_est10:*          53: em_esthum19:*
 11: gb_est11:*          54: em_esthum20:*
 12: gb_est12:*          55: em_esthum21:*
 13: gb_est13:*          56: em_esthum22:*
 14: gb_est14:*          57: em_esthum23:*
 15: gb_est15:*          58: em_esthum24:*
 16: gb_est16:*          59: em_esthum25:*
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 18: gb_est18:*          61: em_esthum27:*
 19: gb_est19:*          62: em_esthum28:*
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 23: gb_est23:*          66: em_estin4:*
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234: gb_gss34:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB ID	Description
	1	5.4	60.0	12	113 AW250557	AW250557 2821633.5
	2	4.8	53.3	11	60 HSM007328	AL042478 Homo sapi
c	3	4.8	53.3	11	60 HSM007344	AL042494 Homo sapi
c	4	4.8	53.3	11	60 HSM007376	AL042526 Homo sapi
c	5	4.4	48.9	11	60 HSM007328	AL042478 Homo sapi
	6	4.4	48.9	11	60 HSM007344	AL042494 Homo sapi
	7	4.4	48.9	11	60 HSM007376	AL042526 Homo sapi
	8	4.4	48.9	11	113 AW250935	AW250935 2821359.3
c	9	4.4	48.9	11	113 AW250935	AL042554 Homo sapi
c	10	4.4	48.9	12	60 HSM007404	AL042554 Homo sapi
c	11	4.4	44.4	5	213 AQ909961	AQ909961 GSSTc0795
c	12	4.4	44.4	12	60 HSM007404	AQ909961 GSSTc0795
c	13	4.4	44.4	11	112 AW247612	AW247612 2819980.5
c	14	4.4	44.4	9	60 HSM008038	AQ909961 GSSTc0795
c	15	4.4	44.4	11	113 AW250935	AW250935 2821359.3
c	16	4	44.4	12	105 AL047587	AL047587 DKF2p586G
c	17	4	44.4	12	105 AL047587	AL047587 DKF2p586G
	18	3.8	42.2	11	206 AQ445580	AQ445580 GSSTc0040

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RESULT 1
LOCUS       AW250557         12 bp    mRNA            EST       07-JAN-2000
DEFINITION  2821633.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821633 5',
            mRNA sequence.
ACCESSION   AW250557
VERSION     AW250557.1  GI:6593550
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 12)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other_ESTs: 2821633.3prime
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 12 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM7 row: F column: 2.
FEATURES             Location/Qualifiers
     source          1..12
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821633"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT     2 a    1 c    4 g    5 t
ORIGIN
        1 c        4 g        5 t

Qy  1 ttctgag 7
       || ||||
Db  5 TTTTGAG 11

Query Match           60.0%;    Score 5.4;    DB 113;    Length 12;
Best Local Similarity 85.7%;    Pred. No. 1.6e+07;
Matches    6;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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ALIGNMENTS

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c	19	3.8	42.2	12	113	AW250557	AW250557 2821633.5	
c	20	3.8	42.2	12	175	C51419	C51419 C51419 Yuji	
c	21	3.4	37.8	7	60	HSM007412	AL042562 Homo sapi	
c	22	3.4	37.8	10	60	HSM004456	AL039980 Homo sapi	
c	23	3.4	37.8	10	60	HSM007587	AL042737 Homo sapi	
c	24	3.4	37.8	10	112	AW248243	AW248243 2819618.5	
c	25	3.4	37.8	11	60	HSM008167	AL043317 Homo sapi	
c	26	3.4	37.8	11	112	AW245969	AW245969 2822722.3	
c	27	3.4	37.8	11	112	AW247612	AW247612 2819980.5	
c	28	3.4	37.8	11	112	AW247933	AW247933 2820656.3	
c	29	3.4	37.8	11	112	AW249647	AW249647 2819740.3	
c	30	3.4	37.8	11	112	AW249797	AW249797 2819795.3	
c	31	3.4	37.8	11	113	AW250442	AW250442 2822410.3	
c	32	3.4	37.8	12	113	HSM007351	AL042501 Homo sapi	
c	33	3.4	37.8	12	60	HSM007351	AL042501 Homo sapi	
c	34	3.4	37.8	12	60	HSM007936	AL043086 Homo sapi	
c	35	3.4	37.8	12	60	HSM008119	AL043269 Homo sapi	
c	36	3.4	37.8	12	106	AU061224	AU061224 AU061224	
c	37	3.4	37.8	12	112	AW249871	AW249871 2821560.3	
c	38	3.4	37.8	12	112	AW250760	AW250760 2821521.3	
c	39	3.4	37.8	12	113	AW250791	AW250791 2822383.3	
c	40	3.4	37.8	12	201	AQ050979	AQ050979 nbxb004d	
c	41	3.4	37.8	12	201	AW672605	AW672605 2xA Expla	
c	42	3	33.3	4	60	HSM010467	AL045617 Homo sapi	
c	43	3	33.3	4	118	AW672622	AW672622 73C Expla	
c	44	3	33.3	5	60	HSM007310	AL042460 Homo sapi	
c	45	3	33.3	5	60	HSM007310	AL042460 Homo sapi	

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RESULT 2
ID   HSM007328/c   standard; RNA; EST; 11 BP.
XX
AC   AL042478;
XX
SV   AL042478.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434F1721_r1  (from clone DKFZp434F1721)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS; Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No sl sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..11
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434F1721"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; Sites NotI + SalI"
FT                   /clone_lib="DKFZp434F1721"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match           53.3%;    Score 4.8;    DB 60;    Length 11;
Best Local Similarity 75.0%;    Pred. No. 4.2e+07;
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Matches   6;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 ttctgaga 8
            ||| || |
Db   9 TTCCGAAA 2

RESULT   3
HSM007344/c
ID   HSM007344   standard; RNA; EST; 11 BP.
XX
AC   AL042494;
XX
SV   AL042494.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434G1721_r1   (from clone DKFZp434G1721)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key   Location/Qualifiers
FH
FT   source   1..11
FT   /db_xref="taxon:9606"
FT   /organism="Homo sapiens"
FT   /clone="DKFZp434G1721"
FT   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT   DH10B; sites NotI + SalI"
FT   /dev_stage="adult"
FT   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match   53.3%;   Score 4.8; DB 60;   Length 11;
Best Local Similarity   75.0%;   Pred. No. 4.2e+07;
Matches   6;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 ttctgaga 8
            ||| || |
Db   9 TTCCGAAA 2

RESULT   4
HSM007376/c
ID   HSM007376   standard; RNA; EST; 11 BP.
XX
AC   AL042526;
XX
SV   AL042526.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX
DE   Homo sapiens mRNA; EST DKFZp434H0321_r1   (from clone DKFZp434H0321)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key   Location/Qualifiers
FH
FT   source   1..11
FT   /db_xref="taxon:9606"
FT   /organism="Homo sapiens"
FT   /clone="DKFZp434H0321"
FT   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT   DH10B; sites NotI + SalI"
FT   /dev_stage="adult"
FT   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match   53.3%;   Score 4.8; DB 60;   Length 11;
Best Local Similarity   75.0%;   Pred. No. 4.2e+07;
Matches   6;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 ttctgaga 8
            ||| || |
Db   9 TTCCGAAA 2

RESULT   5
HSM007328
ID   HSM007328   standard; RNA; EST; 11 BP.
XX
AC   AL042478;
XX
SV   AL042478.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434F1721_r1   (from clone DKFZp434F1721)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA

```
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..11
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434F1721"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Qy            1 ttctga 6
                ||| ||
Db            3 TTCGGA 8

Query Match             48.9%;  Score 4.4; DB 60; Length 11;
Best Local Similarity   83.3%;           Pred. No. 8e+07;
Matches    5;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;


RESULT  6
HSM007344
ID   HSM007344  standard; RNA; EST; 11 BP.
XX
AC   AL042494;
XX
SV   AL042494.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434G1721_r1  (from clone DKFZp434G1721)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..11
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434G1721"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Qy            1 ttctga 6
                ||| ||
Db            3 TTCGGA 8

Query Match             48.9%;  Score 4.4; DB 60; Length 11;
Best Local Similarity   83.3%;           Pred. No. 8e+07;
Matches    5;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;


RESULT  7
HSM007376
ID   HSM007376  standard; RNA; EST; 11 BP.
XX
AC   AL042526;
XX
SV   AL042526.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434H0321_r1  (from clone DKFZp434H0321)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-11
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..11
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434H0321"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Qy            1 ttctga 6
                ||| ||
Db            3 TTCGGA 8

Query Match             48.9%;  Score 4.4; DB 60; Length 11;
Best Local Similarity   83.3%;           Pred. No. 8e+07;
Matches    5;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;


RESULT  8
AW250935
LOCUS       AW250935       11 bp    mRNA       EST       07-JAN-2000
DEFINITION  2821359 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821359 3',
            mRNA sequence.
```

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ACCESSION   AW250935
VERSION     AW250935.1  GI:6593928
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2821359.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: Robert_Strausberg@nih.gov
            Tel: (301) 496-1550
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 11 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM6 row: J column: 16
            High quality sequence stop: 11.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821359"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT     5 a      1 c      4 g      1 t
ORIGIN
```

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RESULT   9
ID       HSM007404    standard; RNA; EST; 12 BP.
XX
AC       AL042554;
XX
SV       AL042554.1
XX
DT       12-MAR-1999 (Rel. 59, Created)
DT       12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE       Homo sapiens mRNA; EST DKFZp43410921_r1 (from clone DKFZp43410921)
```

```
Query Match      9
Best Local Similarity    48.9%;    Score 4.4;  DB 113;  Length 11;
                         83.3%;    Pred. No. 8e+07;
Matches   5;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    3 ctgaga 8
          | |||
Db    4 CAGGA 9
```

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XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-12
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
DE   Homo sapiens mRNA; EST DKFZp43410921_r1 (from clone DKFZp43410921)
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```
RESULT   10
ID       HSM007404/c    standard; RNA; EST; 12 BP.
XX
AC       AL042554;
XX
SV       AL042554.1
XX
DT       12-MAR-1999 (Rel. 59, Created)
DT       12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE       Homo sapiens mRNA; EST DKFZp43410921_r1 (from clone DKFZp43410921)
XX
KW       EST; expressed sequence tag.
XX
OS       Homo sapiens (human)
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC       Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN       [1]
RP       1-12
RA       Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT       ;
RL       Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL       MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC       Clone from S. Wiemann, sequenced by LMU within the cDNA
CC       sequencing consortium of the German Genome Project
CC       No s1 sequence available
XX
FH       Key             Location/Qualifiers
FH
FT       source          1..12
FT                       /organism="Homo sapiens"
FT                       /db_xref="taxon:9606"
FT                       /clone="DKFZp43410921"
FT                       /clone_lib="434 (synonym; htes3). Vector pSport1; host
FT                       DH10B; sites NotI + SalI"
FT                       /dev_stage="adult"
FT                       /tissue_type="testis"
XX
SQ       Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 other;
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```
Query Match      10
Best Local Similarity    48.9%;    Score 4.4;  DB 60;  Length 12;
                         83.3%;    Pred. No. 8.1e+07;
Matches   5;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 ttctga 6
          ||| ||
Db    2 TTCGGA 7
```

```
CC   This clone is available at the R2PD in Berlin
CC   Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..12
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434I0921"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                    DH10B; sites NotI + SalI"
FT                   /dev_stage="adult"
FT                   /tissue_type="testis"
XX
SQ   Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 other;

Qy     1  ttcctga  6
          ||| ||
Db     8  TTCCGA   3

Query Match      48.9%;    Score 4.4;  DB 60;     Length 12;
Best Local Similarity  83.3%;          Pred. No. 8.1e+07;
Matches  5;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;


RESULT 11
LOCUS       AQ909961       5 bp    DNA        GSS       09-JAN-2001
DEFINITION  GSSTc07954 Trypanosoma cruzi random genomic library Trypanosoma
            cruzi genomic clone G35F18, DNA sequence.
ACCESSION   AQ909961
VERSION     AQ909961.2  GI:9371014
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi.
ORGANISM    Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 5)
AUTHORS     Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
TITLE       A random sequencing approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
JOURNAL     Genome Res. 10 (12), 1996-2005 (2000)
MEDLINE     20568489
COMMENT     On Jul 21, 2000 this sequence version replaced gi:6490291.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
            CP(1650) San Martin, Prov. de BS As. Argentina
            Tel: 54-11-4580-7255 ext 309
            Fax: 54-11-4752-9639
            Email: dsanchez@iib.unsam.edu.ar
            Seq primer: T7
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1..5
                     /organism="Trypanosoma cruzi"
                     /strain="CL-Brener"
                     /db_xref="taxon:5693"
                     /clone="G35F18"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /cell_type="epimastigote"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphoryated
                     HincII site of the vector"
BASE COUNT    4 a    0 c    1 g    0 t
ORIGIN
```

```
Qy     6  agaa  9
          ||||
Db     1  AGAA  4

Query Match      44.4%;    Score 4;  DB 213;    Length 5;
Best Local Similarity  100.0%;        Pred. No. 1.7e+09;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 12
LOCUS       AQ909961/c     5 bp    DNA        GSS       09-JAN-2001
DEFINITION  GSSTc07954 Trypanosoma cruzi random genomic library Trypanosoma
            cruzi genomic clone G35F18, DNA sequence.
ACCESSION   AQ909961
VERSION     AQ909961.2  GI:9371014
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi.
ORGANISM    Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 5)
AUTHORS     Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
TITLE       A random sequencing approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
JOURNAL     Genome Res. 10 (12), 1996-2005 (2000)
MEDLINE     20568489
COMMENT     On Jul 21, 2000 this sequence version replaced gi:6490291.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
            CP(1650) San Martin, Prov. de BS As. Argentina
            Tel: 54-11-4580-7255 ext 309
            Fax: 54-11-4752-9639
            Email: dsanchez@iib.unsam.edu.ar
            Seq primer: T7
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1..5
                     /organism="Trypanosoma cruzi"
                     /strain="CL-Brener"
                     /db_xref="taxon:5693"
                     /clone="G35F18"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /cell_type="epimastigote"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphoryated
                     HincII site of the vector"
BASE COUNT    4 a    0 c    1 g    0 t
ORIGIN

Qy     1  ttct  4
          ||||
Db     4  TTCT  1

Query Match      44.4%;    Score 4;  DB 213;    Length 5;
Best Local Similarity  100.0%;        Pred. No. 1.7e+09;
Matches  4;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 13
ID   HSM008038     standard; RNA; EST; 9 BP.
XX
AC   AL043188;
XX
SV   AL043188.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
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DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp434G22223_r1 (from clone DKFZp434G22223)
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-9
RA   Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No s1 sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum; Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..9
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp434G22223"
FT                   /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT                   DH10B; sites NotI + SalI"
FT                   /dev_stage="adult";
FT                   /tissue_type="testis".
XX
SQ   Sequence 9 BP; 1 A; 1 C; 2 G; 5 T; 0 other;

Query Match        44.4%;        Score 4;   DB 60;   Length 9;
Best Local Similarity  100.0%;   Pred. No. 9.7e+08;
Matches  4;  Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          2 tctg 5
              ||||
Db          1 TCTG 4

RESULT 14
AW247612/c
LOCUS       AW247612       11 bp    mRNA         EST     07-JAN-2000
DEFINITION  2819980.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819980 5',
            mRNA sequence.
ACCESSION   AW247612
VERSION     AW247612.1  GI:6590605
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other_ESTs: 2819980.3prime
            Contact: Robert Strausberg, Ph.D.
            Email: Robert_Strausberg@nih.gov
            Tel: (301) 496-1550
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
```

```
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center;
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 11 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM3  row: A  column: 5.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NIH_MGC_7"
                     /clone="IMAGE:2819980"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      3 a      3 c      4 g      1 t
ORIGIN

Query Match        44.4%;        Score 4;   DB 112;   Length 11;
Best Local Similarity  100.0%;   Pred. No. 1.5e+08;
Matches  4;  Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy          2 tctg 5
              ||||
Db          9 TCTG 6

RESULT 15
AW250935/c
LOCUS       AW250935       11 bp    mRNA         EST     07-JAN-2000
DEFINITION  2821359.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821359 3',
            mRNA sequence.
ACCESSION   AW250935
VERSION     AW250935.1  GI:6593928
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other_ESTs: 2821359.5prime
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution Information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence.
            Low Quality Sequence: Trace file contained 11 contiguous distinct
            peaks following vector sequence.
```

```
              Plate: LLCM6 row: J column: 16
              High quality sequence stop: 11.
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821359"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT     5 a     1 c     4 g     1 t
ORIGIN
             1 c
```

Query Match   44.4%;   Score 4; DB 113; Length 11;
Best Local Similarity   100.0%; Pred. No. 1.5e+08;
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     2 tctg 5
         ||||
Db     7 TCTG 4
```

Search completed: April 21, 2001, 12:34:38
Job time: 4794 sec

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